PCT

RAW SEQUENCE LISTING   DATE: 12/28/2004
PATENT APPLICATION: US/10/518,018   TIME: 11:39:51

Input Set : **A:\seqlst_US.txt**
Output Set: **N:\CRF4\12282004\J518018.raw**

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    3 <110> APPLICANT: Shiraki, Kimiyasu
    4          Kurokawa, Masahiko
    5          Tamura, Yoshitaka
    6          Yamauchi, Koji
    7          Wakabayashi, Hiroyuki
    8          Shin, Kouichirou
   10 <120> TITLE OF INVENTION: Inhibitor of Interleukin-6 Production
   12 <130> FILE REFERENCE: TOYA108.008APC
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/518,018
C--> 14 <141> CURRENT FILING DATE: 2004-12-15
     14 <150> PRIOR APPLICATION NUMBER: PCT/JP2003/015009
W--> 15 2003-11-25
W--> 17 <150> PRIOR APPLICATION NUMBER: JP 2003-45509
   18 <151> PRIOR FILING DATE: 2003-02-24
   20 <160> NUMBER OF SEQ ID NOS: 1
   22 <170> SOFTWARE: PatentIn version 3.1
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ERRORED SEQUENCES

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   25 <211> LENGTH: 612
   26 <212> TYPE: PRT
   27 <213> ORGANISM: Bos taurus
   29 <400> SEQUENCE: 1
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   34 Leu Ser Trp Glu Val Gly Cys Gly Ala Pro Val Pro Leu Val Lys Cys
   35             20                  25                  30
   37 Asp Glu Asn Ser Pro Tyr Arg Thr Ile Thr Gly Asp Cys Asn Asn Arg
   38          35                  40                  45
   40 Arg Ser Pro Ala Leu Gly Ala Ala Asn Arg Ala Leu Ala Arg Trp Leu
   41       50                  55                  60
   43 Pro Ala Glu Tyr Glu Asp Gly Leu Ala Leu Pro Phe Gly Trp Thr Gln
   44 65                  70                  75                  80
   46 Arg Lys Thr Arg Asn Gly Phe Arg Val Pro Leu Ala Arg Glu Val Ser
   47             85                  90                  95
   49 Asn Lys Ile Val Gly Tyr Leu Asp Glu Glu Gly Val Leu Asp Gln Asn
   50             100                 105                 110
   52 Arg Ser Leu Leu Phe Met Gln Trp Gly Gln Ile Val Asp His Asp Leu
   53             115                 120                 125
   55 Asp Phe Ala Pro Glu Thr Glu Leu Gly Ser Asn Glu His Ser Lys Thr
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58 Gln Cys Glu Glu Tyr Cys Ile Gln Gly Asp Asn Cys Phe Pro Ile Met
59 145             150             155             160
61 Phe Pro Lys Asn Asp Pro Lys Leu Lys Thr Gln Gly Lys Cys Met Pro
62             165             170             175
64 Phe Phe Arg Ala Gly Phe Val Cys Pro Thr Pro Pro Tyr Gln Ser Leu
65             180             185             190
67 Ala Arg Glu Gln Ile Asn Ala Val Thr Ser Phe Leu Asp Ala Ser Leu
68             195             200             205
70 Val Tyr Gly Ser Glu Pro Ser Leu Ala Ser Arg Leu Arg Asn Leu Ser
71     210             215             220
73 Ser Pro Leu Gly Leu Met Ala Val Asn Gln Glu Ala Trp Asp His Gly
74 225             230             235             240
76 Leu Ala Tyr Leu Pro Phe Asn Asn Lys Lys Pro Ser Pro Cys Glu Phe
77             245             250             255
79 Ile Asn Thr Thr Ala Arg Val Pro Cys Phe Leu Ala Gly Asp Phe Arg
80             260             265             270
82 Ala Ser Glu Gln Ile Leu Leu Ala Thr Ala His Thr Leu Leu Leu Arg
83             275             280             285
85 Glu His Asn Arg Leu Ala Arg Glu Leu Lys Lys Leu Asn Pro His Trp
86     290             295             300
88 Asn Gly Glu Lys Leu Tyr Gln Glu Ala Arg Lys Ile Leu Gly Ala Phe
89 305             310             315             320
91 Ile Gln Ile Ile Thr Phe Arg Asp Tyr Leu Pro Ile Val Leu Gly Ser
92             325             330             335
94 Glu Met Gln Lys Trp Ile Pro Pro Tyr Gln Gly Tyr Asn Asn Ser Val
95             340             345             350
97 Asp Pro Arg Ile Ser Asn Val Phe Thr Phe Ala Phe Arg Phe Gly His
98             355             360             365
100 Met Glu Val Pro Ser Thr Val Ser Arg Leu Asp Glu Asn Tyr Gln Pro
101     370             375             380
103 Trp Gly Pro Glu Ala Glu Leu Pro Leu His Thr Leu Phe Phe Asn Thr
104 385             390             395             400
106 Trp Arg Ile Ile Lys Asp Gly Gly Ile Asp Pro Leu Val Arg Gly Leu
107             405             410             415
109 Leu Ala Lys Lys Ser Lys Leu Met Asn Gln Asp Lys Met Val Thr Ser
110             420             425             430
112 Glu Leu Arg Asn Lys Leu Phe Gln Pro Thr His Lys Ile His Gly Phe
113             435             440             445
115 Asp Leu Ala Ala Ile Asn Leu Gln Arg Cys Arg Asp His Gly Met Pro
116     450             455             460
118 Gly Tyr Asn Ser Trp Arg Gly Phe Cys Gly Leu Ser Gln Pro Lys Thr
119 465             470             475             480
121 Leu Lys Gly Leu Gln Thr Val Leu Lys Asn Lys Ile Leu Ala Lys Lys
122             485             490             495
124 Leu Met Asp Leu Tyr Lys Thr Pro Asp Asn Ile Asp Ile Trp Ile Gly
125             500             505             510
127 Gly Asn Ala Glu Pro Met Val Glu Arg Gly Arg Val Gly Pro Leu Leu
128             515             520             525
130 Ala Cys Leu Leu Gly Arg Gln Phe Gln Gln Ile Arg Asp Gly Asp Arg
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131       530                   535                   540
133 Phe Trp Trp Glu Asn Pro Gly Val Phe Thr Glu Lys Gln Arg Asp Ser
134 545                   550                   555                   560
136 Leu Gln Lys Val Ser Phe Ser Arg Leu Ile Cys Asp Asn Thr His Ile
137                   565                   570                   575
139 Thr Lys Val Pro Leu His Ala Phe Gln Ala Asn Asn Tyr Pro His Asp
140                   580                   585                   590
142 Phe Val Asp Cys Ser Thr Val Asp Lys Leu Asp Leu Ser Pro Trp Ala
143                   595                   600                   605
145 Ser Arg Glu Asn
146            610
E--> 147  ??
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VERIFICATION SUMMARY   DATE: 12/28/2004
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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:15 M:259 W: Allowed number of lines exceeded, <150> PRIOR APPLICATION NUMBER:
L:17 M:289 W: Identifier Missing or Out-Of-Order, <150> PRIOR APP FILING DATE
L:147 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:147 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:149 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:149 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:149 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
M:332 Repeated in SeqNo=1
L:151 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:151 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:153 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:153 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1